

10/540092

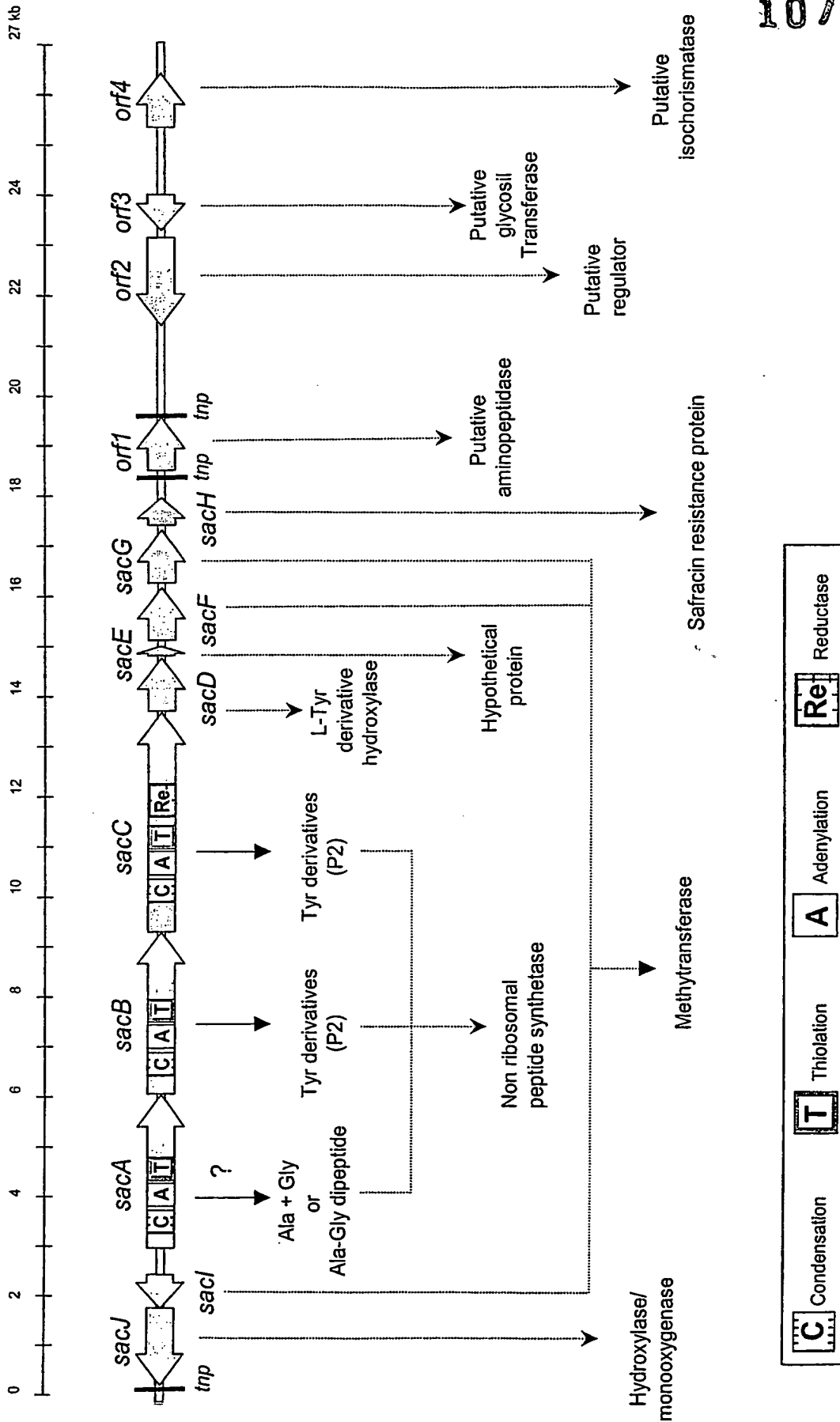


Figure 1

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Core	1	2	3	4	5	6
Sequence	LKAGGA	SGTTG	GELCIGG	TGD	RIELGEIE	LGGHS
SafB1 97	-LYAGVAVPVYP-78	-YTSGSTADPKG-220	-GEIWVRGPSVAQGY-23	-LRTGDL-23	-NYYPQDLEL-163	-LPDLGLDSLALVELKHRIE-
SafB2 1247	-LEAGGVAVPLDP-64	-YTSGSTGQPKG-172	-GELFIGGAGVARGY-24	-YRTGDL-23	-FRIEFEEIE-121	-FFDLGGNSLLATRLATRLA-
SafA1 559	-LKAGGAYVPLDP-64	-YTSGSSGRPKG-173	-GELFIGGSGVARGY-24	-YRTGDL-23	-YRIELAEIE-121	-FFELGGNSLLAGRLVEELD-
SafA2 1668	-LKAGGAYVPLDP-67	-YTSGSTGTPKA-179	-GELFVGGVGLARGY-24	-YRTGDL-23	-YRVELGEIE-122	-FFEVGGTSLLLARLASRL-
SacA 483	-MACGGSYVPLSD-63	-FTSGSTGEPKG-172	-GELIIHGHGVAQGY-20	-YRTGDR-23	-FRVELGPVQ-121	-FLDIGGHSLSLTLTGILR-
SacB 524	-WQVGGIYVPLSK-63	-YTSGSTGKPKG-173	-GELLICGPGVSQGY-22	-YLTGDR-23	-HRIELGEIE-123	-FFQLGGHSILVARMVERIE-
SacC 515	-RAGHAFLPIDDR-62	-YTSGSTGVPKG-178	-GEIMLAGQNLARGY-21	-YATGDL-23	-HRIELNEVA-122	-FFEQGGNSILLTLTLAGTLS-
FUNCTION	unknown	ATP binding	ATP binding	ATPase motif	ATP binding	4' phosphopantetheine binding

Figure 2

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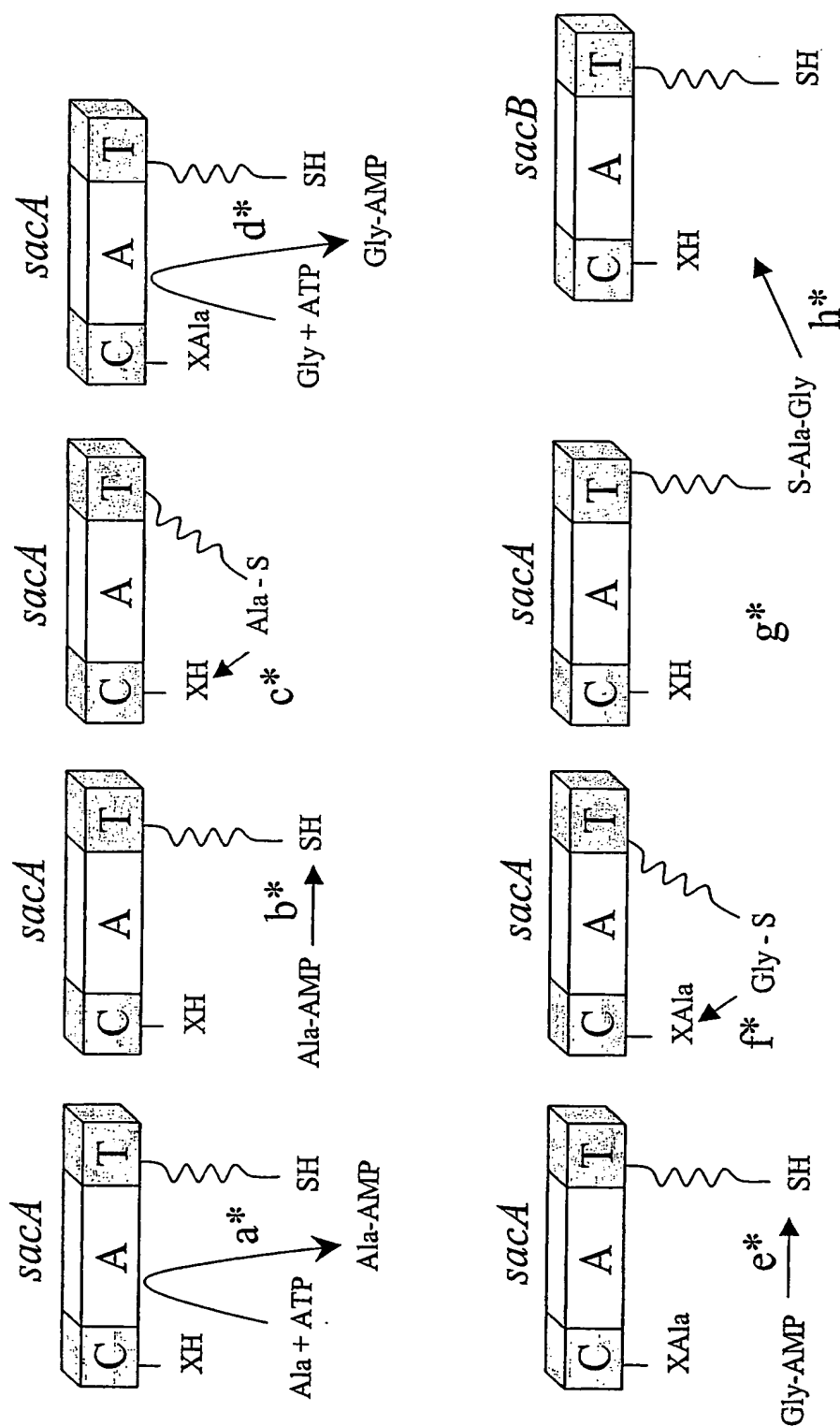


Figure 3

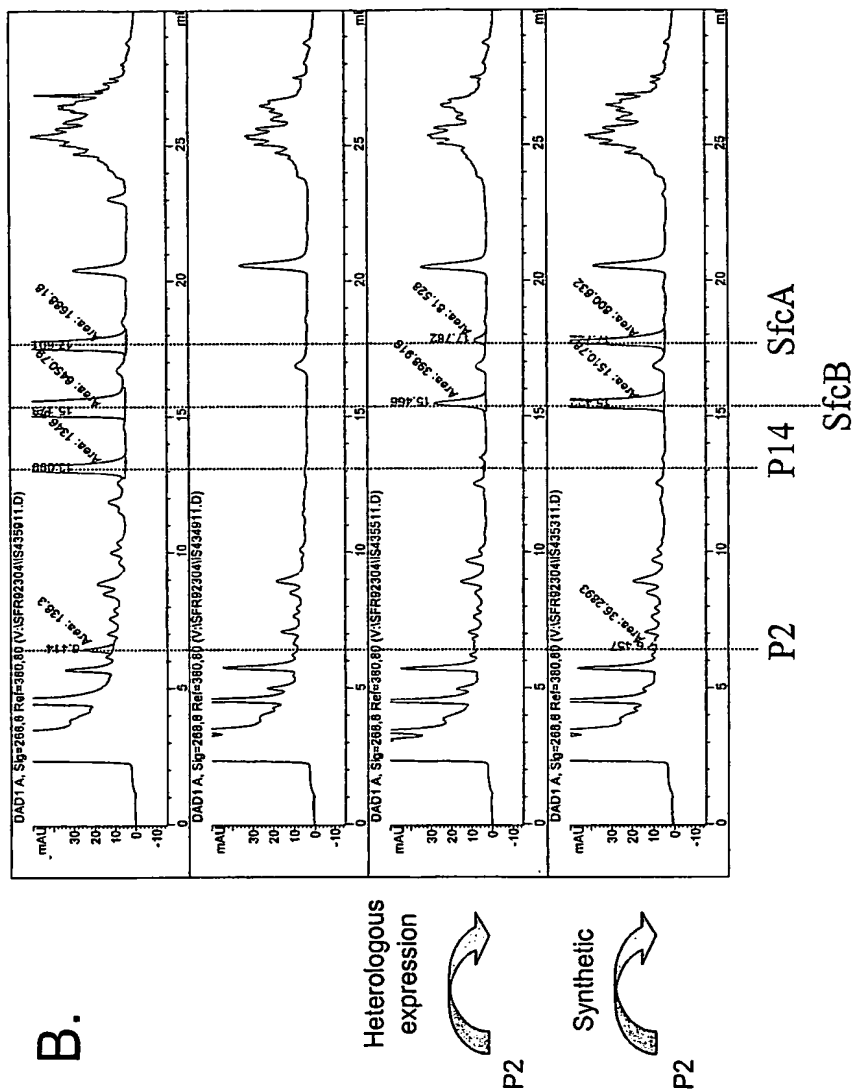
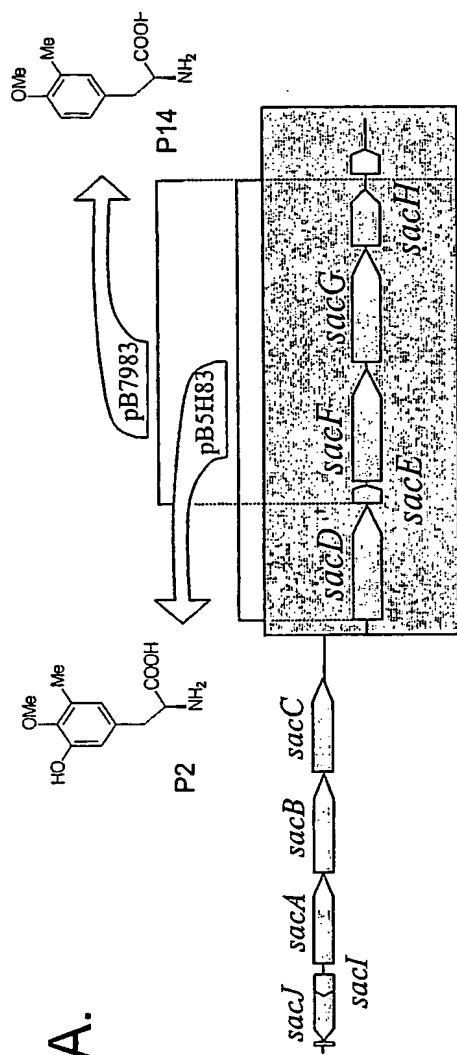


Figure 4

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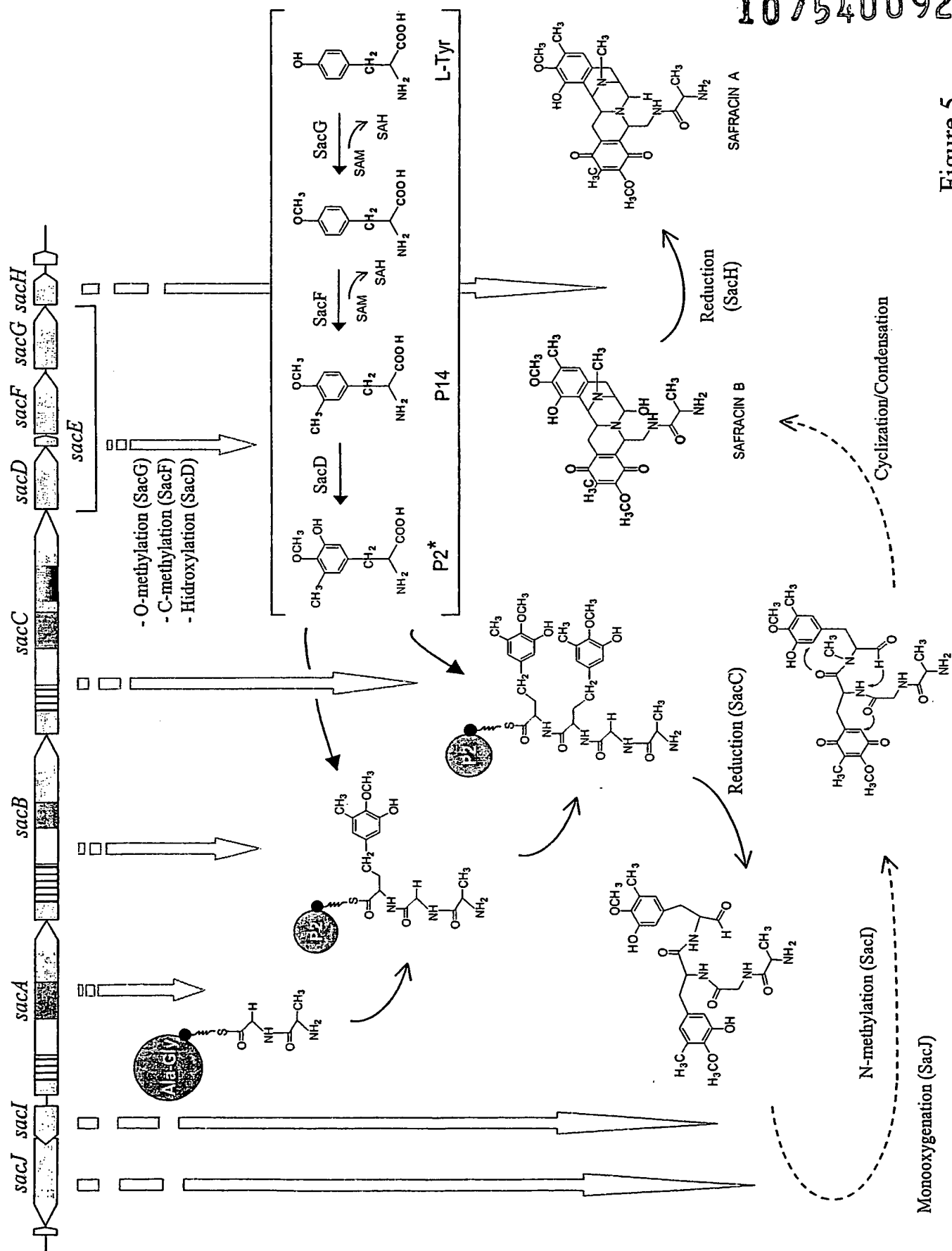


Figure 5

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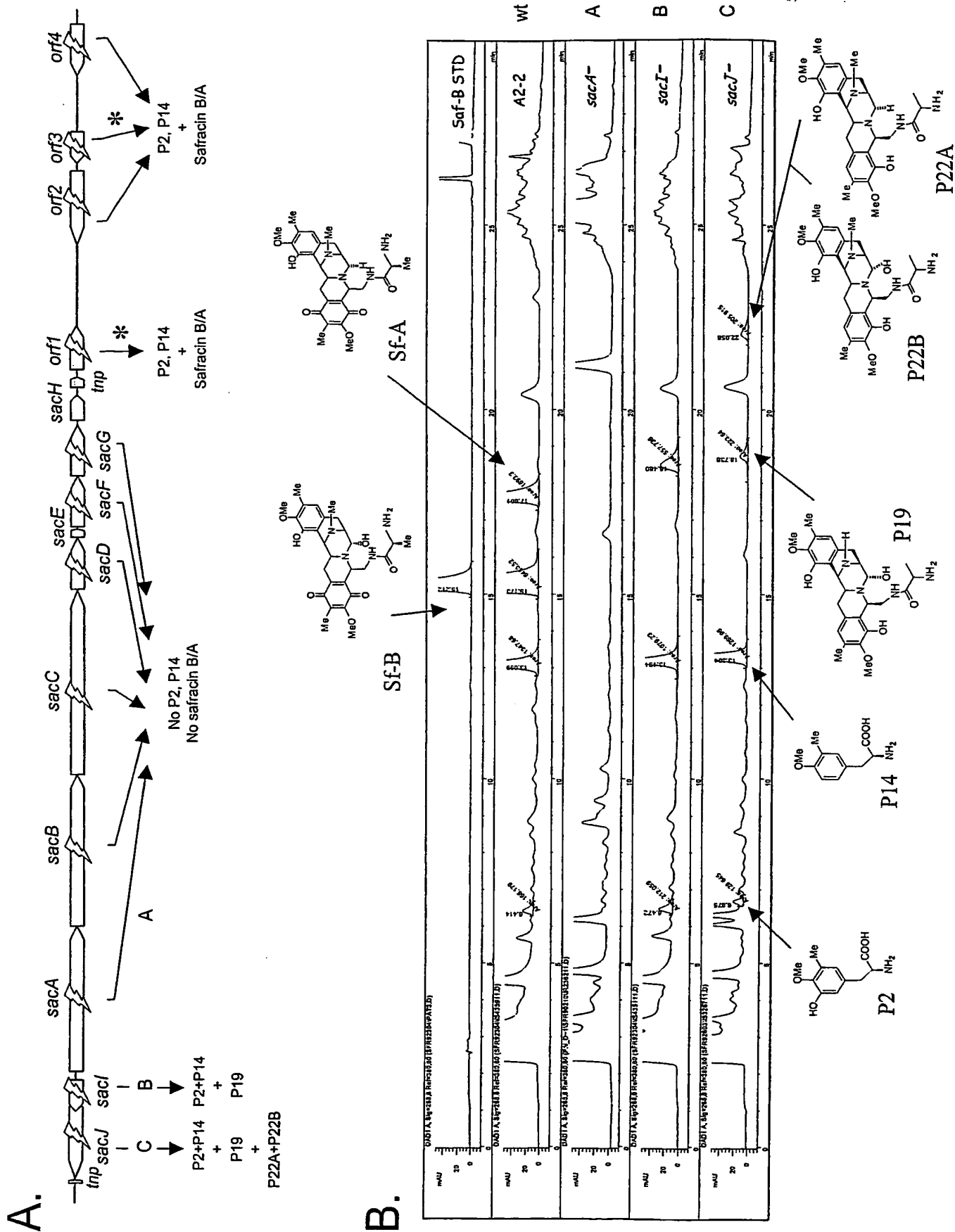


Figure 6

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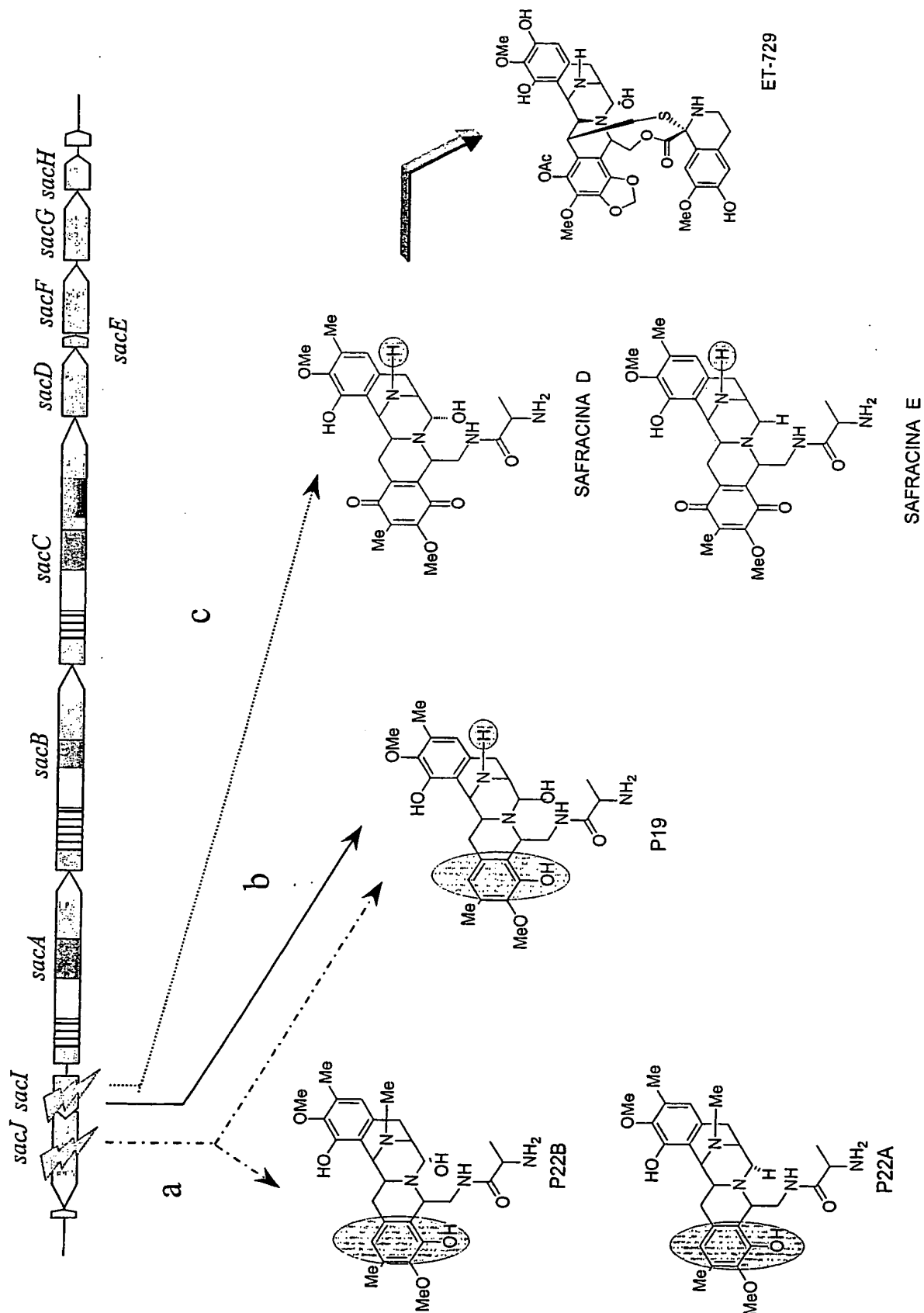


Figure 7

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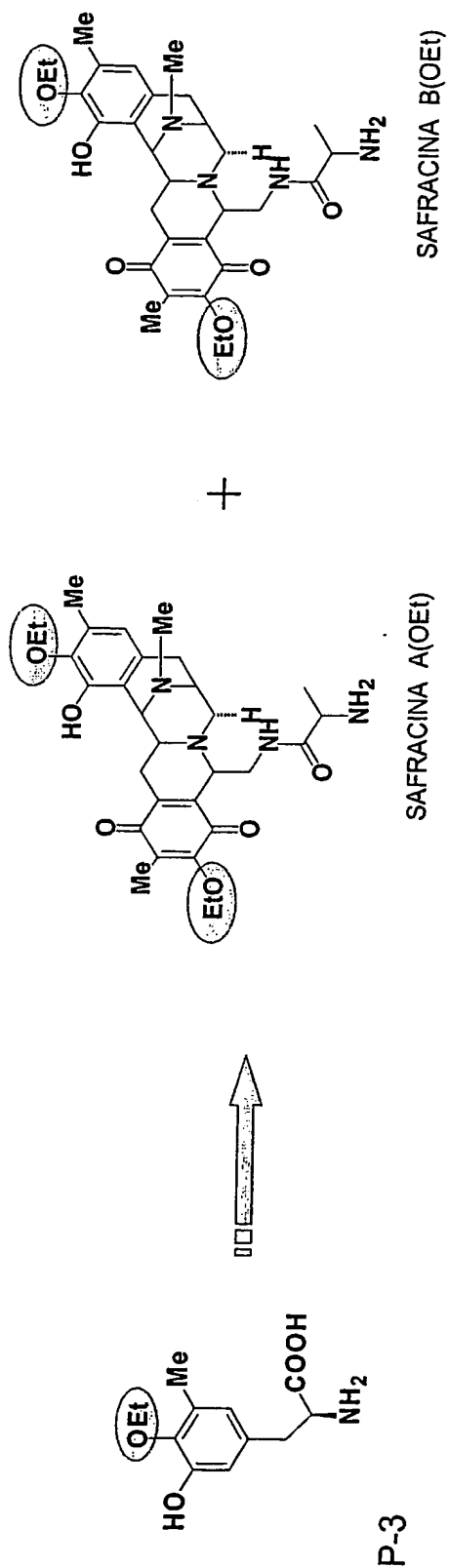


Figure 8

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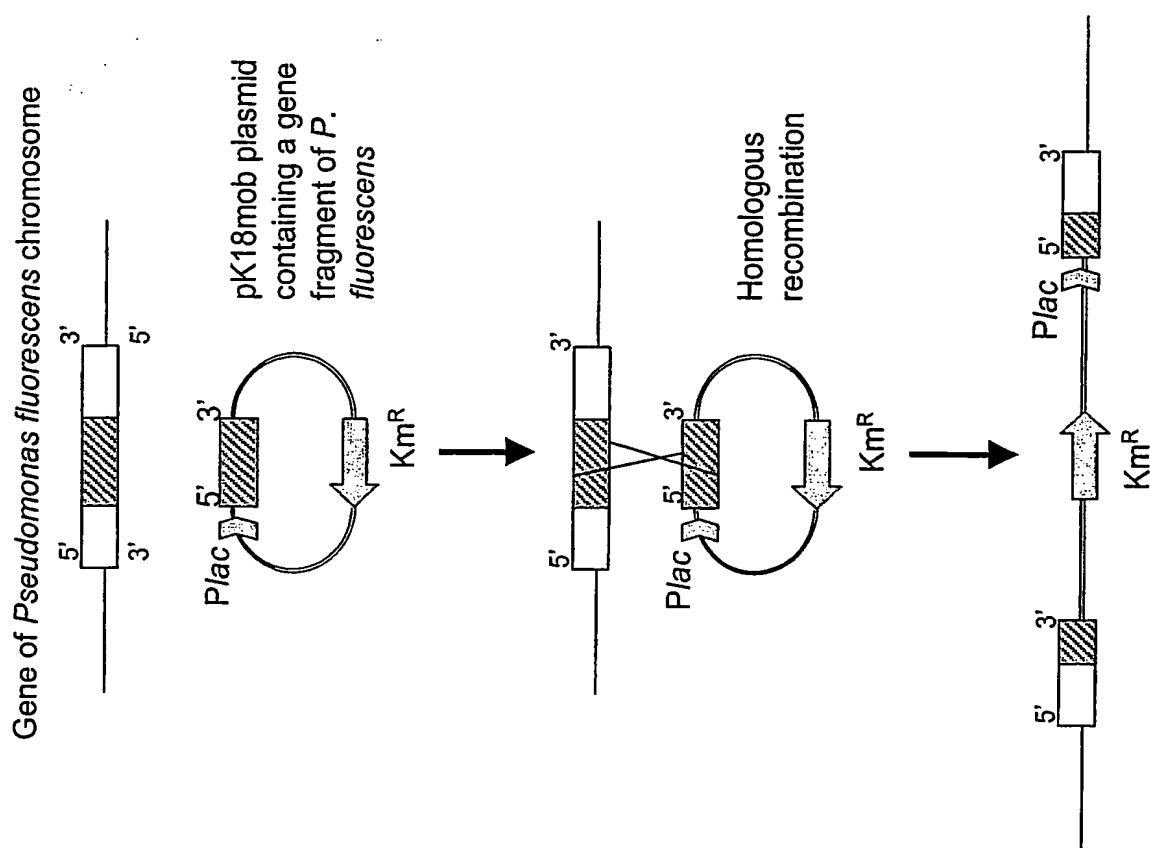


Figure 9